

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2001, 12:06:13 ; Search time 16.04 Seconds
(without alignments)
1491.198 Million cell updates/sec

Title: US-09-486-334-2
Perfect score: 1641
Sequence: 1 MATCIDTCRTGNTQDDSRF.....IPCLTMDQTSYLTMSDYVI 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1641	100.0	314	2	S67482
2	1611	98.2	314	2	S71181
3	1215	74.0	391	2	S69192
4	1105	67.3	303	2	S68469
5	877	53.4	347	2	T09140
6	869	51.8	294	2	A57478
7	849.5	51.0	312	2	S71207
8	699	42.6	315	2	F84554
9	649.5	39.6	272	2	C81184
10	648.5	39.5	273	1	XRECSA
11	648.5	39.5	273	2	S29568
12	648.5	39.5	273	2	F86036
13	647.5	39.5	273	2	G82049
14	643	39.2	308	2	T08867
15	624.5	38.1	267	2	G64080
16	587.5	35.8	299	2	T04669
17	573.5	34.9	274	2	A84936
18	549.5	33.5	261	1	UC1293
19	472.5	28.8	270	2	T50058
20	442	26.9	225	1	B53402
21	424	25.8	217	1	H53402
22	422.5	25.7	227	2	T44913
23	420.5	25.6	249	1	S75606
24	409	24.9	251	2	T44279
25	405	24.7	229	2	H70660
26	395	24.1	229	2	F83663
27	392	23.9	258	2	A83169
28	389.5	23.7	199	2	E86856
29	388.5	23.7	212	2	C81347

30	369.5	22.5	269	1	D43706	serine O-acetyl
31	365	22.2	171	1	B64671	serine O-acetyl
32	359	21.9	171	2	B71845	o-serine acetyl
33	359	20.6	220	2	G72349	serine acetyl
34	312	19.0	171	2	D84302	serine acetyl
35	287	17.5	319	2	S55322	srp protein - Syn
36	265	16.1	231	2	A64972	probable acetyl
37	217	13.2	162	2	A83381	probable acetyl
38	217	13.2	184	2	B85832	serine acetyl
39	207	12.6	184	2	C82264	serine acetyl
40	179	10.9	256	2	A86660	serine acetyl
41	177.5	10.8	143	2	G82264	serine acetyl
42	175	10.7	236	2	H72245	serine acetyl
43	175	10.7	240	2	B83983	tetracycline
44	171	10.4	201	2	H85806	hypothetical prote
45	164.5	10.0	190	2	S07000	modulation protein

ALIGNMENTS

RESULT 1
S67482
serine O-acetyltransferase (EC 2.3.1.30), cytosolic - Arabidopsis thaliana
N:Alternate names: serine acetyltransferase
C:Species: Arabidopsis thaliana (mouse ear cress)
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000
C:Accession: S67482; S52150
R:Ruffet, M.L.; Lebrun, M.; Droux, M.; Douce, R.
Eur. J. Biochem. 227, 500-509, 1995
A:Title: Subcellular distribution of serine acetyltransferase from Pisum sativum and
A:Reference number: S67482; MID:95154333
A:Accession: S67482
A:Molecule type: DNA
A:Residues: 1-314 <RUF>
A:Cross-references: EMBL:Z34888; NID:9608676; PIDN:TA84371.1; PID:9608677
A:Note: the authors translated the codon ACC for residue 158 as Ile and ACA for resid
C:Superfamily: serine acetyltransferase; serine acetyltransferase homology
C:Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F:123-283/Domain: serine acetyltransferase homology <SMT>

Query Match	100.0%; Score 1641; DB 2; Length 314;
Best Local Similarity	100.0%; Pred. No. 8.8e-129; Indels 0;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MATCIDTCRTGNTQDDSRFCCINFRPGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60	
DB 1 MATCIDTCRTGNTQDDSRFCCINFRPGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60	
QY 61 KOEPLISNYYVASTSHRSLSALAHILSVKLSNMLPSNTFELFISYLESPETTEST 120	
DB 61 KOEPLISNYYVASTSHRSLSALAHILSVKLSNMLPSNTFELFISYLESPETTEST 120	
QY 121 KODLAVKRPDPAISYVHCFGFGFLACQAHRIATHLQKNNKIYALLIQNRVSESA 180	
DB 121 KODLAVKRPDPAISYVHCFGFGFLACQAHRIATHLQKNNKIYALLIQNRVSESA 180	
QY 181 VDIHPKAKIGKGLDHAATGAVIGETAVVGDVNSILHGVLTGSGKSGRHRKIGDYL 240	
DB 181 VDIHPKAKIGKGLDHAATGAVIGETAVVGDVNSILHGVLTGSGKSGRHRKIGDYL 240	
QY 241 IGAGSCILGNTTIGEGAKIGSGSVYKVPATTAIVGNPRLIGGKPNRKHKIPCLTW 300	
DB 241 IGAGSCILGNTTIGEGAKIGSGSVYKVPATTAIVGNPRLIGGKPNRKHKIPCLTW 300	
QY 301 DQTSYLTMSDYVI 314	
DB 301 DQTSYLTMSDYVI 314	
RESULT 2	
S71181	

serine O-acetyltransferase (EC 2.3.1.30) SAT precursor, chloroplast - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000
 C:Accession: S71181
 R:Murillo, M.; Foglia, R.; Diller, A.; Leustek, T.
 Submitted to the EMBL Data Library, August 1995
 A:Description: Analysis of a cDNA encoding serine acetyltransferase from Arabidopsis thaliana of Escherichia coli.
 A:Reference number: S71181
 A:Accession: S71181
 A:Molecule type: mRNA
 A:Residues: 1-314 <MR>
 A:Cross-references: EMBL:L42212; NID:9926938; PIDN:AAC37474.1; PID:9926939
 A:Note: probably chloroplast isoform; no transit peptide given
 C:Genetics:
 A:Superfamily: serine acetyltransferase; serine acetyltransferase homology
 A:Keywords: acyltransferase; chloroplast; coenzyme A; cysteine biosynthesis
 F:123-283/Domain: serine acetyltransferase homology <SAT>

Query Match 98.2%; Score 1611; DB 2; Length 314;
 Best Local Similarity 98.1%; Pred. No. 2, 7e-126;
 Matches 308; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MATCIDTCRTGNTQDDSRFCCKNFPRGFSVNRKIHHTQIEDDDWIKMLEAKSDY 60
 Db 1 MATCIDTCRTGNTQDDSRFCCKNFPRGFSVNRKIHHTQIEDDDWIKMLEAKSDY 60
 QY 61 KOEPIISNYVYASTSHRSLESALAHILSVKLSNLTPELFIYVLESEPIITST 120
 Db 61 KOEPIISNYVYASTSHRSLESALAHILSVKLSNLTPELFIYVLESEPIITST 120
 QY 121 KODLIWVKERDPACISYVCFEGFKGLACQAHRIAHITLQNKRIYALLQNRVSEFA 180
 Db 121 KODLIWVKERDPACISYVCFEGFKGLACQAHRIAHITLQNKRIYALLQNRVSEFA 180
 QY 181 VDIHPGAKIGKGIILDHATGVIGTAVGDNVSLIHVTIGGFGKSGDRHPKIGDVL 240
 Db 181 VDIHPGAKIGKGIILDHATGVIGTAVGDNVSLIHVTIGGFGKSGDRHPKIGDVL 240
 QY 241 IGAGSIIICNTITIGGAKIGSGSVVKKDVPARTAVGNPARIIGKKNPKHKDIPCLTM 300
 Db 241 IGAGSIIICNTITIGGAKIGSGSVVKKDVPARTAVGNPARIIGKKNPKHKDIPCLTM 300
 QY 301 DOTSYLTEMSDYVI 314
 Db 301 DOTSYLTEMSDYVI 314

RESULT 3
 S69192
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 05-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 05-May-2000
 C:Accession: S69192; S71906
 R:Roberts, M.A.; Wray, J.L.
 Plant Mol. Biol. 30, 1041-1049, 1996
 A:Title: Cloning and characterization of an Arabidopsis thaliana cDNA clone encoding an
 A:Reference number: S69192; MUID:96270381
 A:Accession: S69192
 A:Molecule type: mRNA
 A:Residues: 1-391 <ROB>
 A:Cross-references: EMBL:U22964; NID:g1184047; PIDN:AA807778.1; PID:g1184048
 R:Hell, R.
 Submitted to the EMBL Data Library, July 1995
 A:Reference number: S71906
 A:Accession: S71906
 A:Molecule type: mRNA
 A:Residues: 80-391 <HEL>
 A:Cross-references: EMBL:X82888; NID:9897677; PIDN:CAA58061.1; PID:9897678
 A:Genetics:
 A:Genome: nuclear

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology
 C:Keywords: acyltransferase; chloroplast; coenzyme A; cysteine biosynthesis
 F:1-60/Domain: transit peptide (chloroplast) #status predicted <TRP>
 F:61-391/Product: serine O-acetyltransferase SAT-1a, chloroplast #status predicted <M
 F:200-360/Domain: serine acetyltransferase homology <SAT>

Query Match 74.0%; Score 1215; DB 2; Length 391;
 Best Local Similarity 72.0%; Pred. No. 2, 9e-93;
 Matches 242; Conservative 31; Mismatches 41; Indels 22; Gaps 4;
 QY 1 MATCIDTCRTGNTQDDSRFCCKNFPRGFSVNRKIHHTQIEDDDWIKMLEAKSDY 60
 Db 1 MATCIDTCRTGNTQDDSRFCCKNFPRGFSVNRKIHHTQIEDDDWIKMLEAKSDY 60
 QY 45 DDDWIKMLEAKSDYKOEPIISNYVYASTSHRSLESALAHILSVKLSNLTPELFI 115
 Db 45 DDDWIKMLEAKSDYKOEPIISNYVYASTSHRSLESALAHILSVKLSNLTPELFI 115
 QY 116 LDRDAEYDVWAKIREAKSDIAKEPIVSAVYHASTVSKLEALANTLSVKLSNLTLP 175
 Db 116 LDRDAEYDVWAKIREAKSDIAKEPIVSAVYHASTVSKLEALANTLSVKLSNLTLP 175
 QY 99 SNTLFEIISVLESEPIITSTKODLIWVKERDPACISYVCFEGFKGLACQAHRIAH 158
 Db 99 SNTLFEIISVLESEPIITSTKODLIWVKERDPACISYVCFEGFKGLACQAHRIAH 158
 QY 176 SNTLFEIISVLESEPIITSTKODLIWVKERDPACISYVCFEGFKGLACQAHRIAH 235
 Db 176 SNTLFEIISVLESEPIITSTKODLIWVKERDPACISYVCFEGFKGLACQAHRIAH 235
 QY 159 LMKQNKRIYALLQNRVSEFAVDIHPGAKIGKGIILDHATGVIGTAVGDNVSLIH 218
 Db 159 LMKQNKRIYALLQNRVSEFAVDIHPGAKIGKGIILDHATGVIGTAVGDNVSLIH 218
 QY 219 VTLGFGKSGDRHPKIGSGVILGAGSCTIGNTTIGGAKIGSGSVVKKDVPARTAVGN 278
 Db 219 VTLGFGKSGDRHPKIGSGVILGAGSCTIGNTTIGGAKIGSGSVVKKDVPARTAVGN 278
 QY 296 VTLGFGKSGDRHPKIGSGVILGAGSCTIGNTTIGGAKIGSGSVVKKDVPARTAVGN 355
 Db 296 VTLGFGKSGDRHPKIGSGVILGAGSCTIGNTTIGGAKIGSGSVVKKDVPARTAVGN 355
 QY 279 PARLIGKKNPKHKDIPCLTMDSYTEMSDYVI 314
 Db 279 PARLIGKKNPKHKDIPCLTMDSYTEMSDYVI 314
 QY 356 PARLIGKKNPKHKDIPCLTMDSYTEMSDYVI 391
 Db 356 PARLIGKKNPKHKDIPCLTMDSYTEMSDYVI 391

RESULT 4
 S68469
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
 C:Accession: S68469
 R:Bogdanova, N.; Bork, C.; Hell, R.
 FEBS Lett. 358, 43-47, 1995
 A:Title: Cysteine biosynthesis in plants: isolation and functional identification of
 A:Reference number: S68469; MUID:95121457
 A:Accession: S68469
 A:Molecule type: mRNA
 A:Residues: 1-303 <BOG>
 A:Cross-references: EMBL:X82888
 C:Genetics:
 A:Superfamily: serine acetyltransferase; serine acetyltransferase homology
 A:Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
 F:113-272/Domain: serine acetyltransferase homology <SAT>

Query Match 67.3%; Score 1105; DB 2; Length 303;
 Best Local Similarity 73.0%; Pred. No. 2, 8e-84;
 Matches 222; Conservative 30; Mismatches 36; Indels 16; Gaps 6;
 QY 25 NFRYDGRSFGNCTQKTLHTRPLEDLDRDAEYDVWAKIREAKSDIAKEPIVSAVYH 71
 Db 25 NFRYDGRSFGNCTQKTLHTRPLEDLDRDAEYDVWAKIREAKSDIAKEPIVSAVYH 71
 QY 72 ASITSHRSLESALAHILSVKLSNLTPELFIYVLESEPIITSTKODLIWVKERD 131
 Db 72 ASITSHRSLESALAHILSVKLSNLTPELFIYVLESEPIITSTKODLIWVKERD 131
 QY 62 ASIVSQSTLEALANTLSVKLSNLTPELFIYVLESEPIITSTKODLIWVKERD 121
 Db 62 ASIVSQSTLEALANTLSVKLSNLTPELFIYVLESEPIITSTKODLIWVKERD 121
 QY 132 PACISYVCFEGFKGLACQAHRIAHITLQNKRIYALLQNRVSEFAVDIHPGAKIGT 191
 Db 132 PACISYVCFEGFKGLACQAHRIAHITLQNKRIYALLQNRVSEFAVDIHPGAKIGT 191

QY	48	WMKLEBAKSDVQOEPILSNYAYATSHRSRSESALAH1SVKXSLNLSNPNTLEFELP1	10
		: : : : : : : : : : : : : : : : : : : : : :	
Db	45	LMTOIKARADAEAPALASVLTSTLSSLSERSISTRIJONKLCOSSTLSTLTYDLEFL	10
QY	108	SVLESPETIESTKODLIAYEKRPDACSIVYHCFLEFKGIJACQAHRIAHLTWKONKRTIV	16
		: : : : : : : : : : : : : : : : : : : : : :	
Db	105	NIFSSDPFLRNATYAADLRAARVRDPACISFHCLLNWKGIJAOAHRSVSHKLMTOSRPL	16
		: : : : : : : : : : : : : : : : : : : : : :	
QY	168	ALLIONRVSESPAVDHPHGAKITGKILLDRATGVIGETVAGDNYSILHGTVLGGTGKO	22
		: : : : : : : : : : : : : : : : : : : : : :	
Db	165	ALATLSRISIDYFAVDIHPHAAITGKILLDRATGVVGETVIGSNVSIILHHTVLGGTGKA	22
		: : : : : : : : : : : : : : : : : : : : : :	
QY	228	SGDRHPKITGDGVLIGAGSCILGNITTEGAKIGGSSVYVHJVPARTAVGNPAPRLIGGKE	28
Db	225	GDRAHPKITDGLITGAGTILGNKITAGAKVAGGGSVYLTVPCRGAVGNPAPRLIGGKE	28

OY 288 NPRKHD-KIPCLTMDOTSLTMSDYVI 314
 Db 285 KPTIHDECPGSGSMHTSFISEMSDYII 312

RESULT 8

probable serine O-acetyltransferase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: F84554
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 Nuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: F84554
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-315 <STO>
 A:Cross-references: GB:AE002093; NID:96598796; PIDN:AAF18673.1; GSPDB:GNO0139
 C:Genetics:
 A:Gene: At2g1640
 A:Map position: 2

Query Match 42.6%; Score 699; DB 2; Length 315;
 Best Local Similarity 50.2%; Pred. No. 1.6e-50;
 Matches 141; Conservative 50; Mismatches 76; Indels 14; Gaps 4;

OY 27 FRGEFSNRR-IHHTQEDD-----DYYWKMLEAKSDVKOEPLSNYYVASTSHRS 79
 Db 8 FESGFEYVAGTKHSESDSNLDPKSDPIWDAIREAK--LEKEPILSGFLVAGLHADC 65
 OY 80 LESALHILSVKLSNLTSPNLTFLFISVLESPELIESTMODLIANKERDPACISVH 139
 Db 66 LEQALGFVLANRLQNTFLATQLOLDFYGVMMHDKIGSSIRHDIQARKDRPACISYS 125
 OY 140 CFIQFGFGLACQAHRIAHFLMKONKRIYALLIQNRVSEFAVDIHPGAKIGKIGLIDHAT 199
 Db 126 AILHLKGYHALQAYRAVHKLWNEGRKLLALQSRISSEVFGIDIPARIEGILLDHGT 185
 OY 200 GVVGSTAVAGDNVSLIHGVTGSGKSGDHPKIGGCVILGAGSCILNITTEGAKI 259
 Db 186 GVVGSTAVAGDNVSLIHGVTGSGKSGDHPKIGGCVILGAGSCILNITTEGAKI 259
 OY 260 GSGSVVAVKVPARTAVGNPARLIGKKNPKRHKIPCLITM 300
 Db 246 AAGSLVLKDVPSHVSAGNPALKIRVME-----EGDPSLAM 281

RESULT 9

probable serine O-acetyltransferase (EC 2.3.1.30) NMA0742 [imported] - Neisseria meningitidis
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
 C:Accession: C81184; H81917
 R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;
 Hickley, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlata, V.; Masiarant, V.; Pizsa, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755
 A:Accession: C81184
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-272 <TEI>
 A:Cross-references: GB:AE002412; GB:AE002098; NID:97225783; PIDN:AAF40988.1; PID:9722578
 A:Experimental source: serogroup B, strain MC58
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491
 A:Reference number: A81775; MUID:20222556
 A:Accession: H81917
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-272 <PAR>
 A:Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CAB84026.1; PID:9737

A:Experimental source: serogroup A, strain 22491

A:Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CAB84026.1; PID:9737
 C:Superfamily: serine acetyltransferase; serine acetyltransferase homology
 C:Keywords: acyltransferase; coenzyme A
 F:88-248/Domain: serine acetyltransferase homology <SAT>

A:Gene: cysE; NMB0560; NMA0742

A:Experimental source: serogroup A, strain 22491
 C:Superfamily: serine acetyltransferase; serine acetyltransferase homology
 C:Keywords: acyltransferase; coenzyme A
 F:88-248/Domain: serine acetyltransferase homology <SAT>

Query Match

39.6%; Score 649.5; DB 2; Length 272;
 Best Local Similarity 50.7%; Pred. No. 1.7e-46;
 Matches 136; Conservative 39; Mismatches 86; Indels 7; Gaps 2;

OY 47 DWITKMLEAKSDVKOEPLSNYYVASTSHRSLEBALHILSVKLSNLTSPNLTFLF 106
 Db 12 DWHTTIEETAAVSAEPMPLASFLHQTIVLRHESLGSVLAHLSKIGSPIMDVRAFELY 71
 OY 107 ISVLESPELIESTMODLIANKERDPACISVYHCFGFK:FLACQAHRIAHFLMKONKI 166
 Db 72 QQALGSTQIGKCEVADLKAIRYERDPACDEYSLPLIFKCFALDHNHNLIDYDGRKT 131
 OY 167 VALLIONRSEFAVDIHPGAKIGKIGLIDHATGVIGETAVAGDNVSLHGLVLTGSGTK 226
 Db 132 LAFLQNRSEVFGVHHPARFGYGLMDHATGVAGETAVLGNISILHGLVLTGSGTK 191
 OY 227 QSGDRHPRKIGDGLVILGAGSCILNITIGEGAKIGSGSVVAVKVPARTAVGNPARLIGK 286
 Db 192 EGGDRHPRKIGDGLVILGAGSCILNITIGEGAKIGSGSVVAVKVPARTAVGNPARLIGK 286
 OY 287 ENRKRHKIPCLTMDOTSLTMSDYVI 314
 Db 250 ----NSLKTSPADMDONIQFTE-IDFMI 272

RESULT 10

serine O-acetyltransferase (EC 2.3.1.30) - Escherichia coli
 C:Species: Escherichia coli
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 05-May-2000
 C:Accession: A27896; A34563; S47828; A65161
 R:Denk, D.; Bock, A.
 J. Gen. Microbiol. 133, 515-525, 1987
 A:Title: L-Cysteine biosynthesis in Escherichia coli: nucleotide sequence and express
 A:Reference number: A27896; MUID:88009872
 A:Accession: A27896
 A:Molecule type: DNA
 A:Residues: 1-273 <DEN>
 A:Cross-references: GB:M15745; NID:9145675; PIDN:AA23648.1; PID:9145676
 R:Tei, H.; Murata, K.; Kimura, A.
 Biochem. Biophys. Res. Commun. 167, 948-955, 1990
 A:Title: Structure and expression of cysX, the second gene in the Escherichia coli K-
 A:Reference number: A34563; MUID:90211342
 A:Accession: A34563
 A:Molecule type: DNA
 A:Residues: 1-273 <TEI>
 A:Cross-references: GB:M34333; NID:9145693; PIDN:AAA23659.1; PID:9145694
 R:Plunkett, G.
 submitted to the EMBL Data Library, March 1994
 A:Reference number: A47666
 A:Accession: S47666
 A:Molecule type: DNA
 A:Residues: 1-273 <PIU>
 A:Cross-references: EMBL:U00039; NID:9466582; PIDN:AA318584.1; PID:9466745
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: A65161

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-273 <BLAT>

A:Cross-references: GB:AE000438; GB:U00096; NID:92367251; PIDN:AAC76631.1; PID:q1790035;

A:Experimental source: strain K-12, substrain MG1655

A:Comment: This enzyme catalyzes the conversion of L-serine to O-acetyl serine (by acetyl

C:Genetics:

A:Gene: *cysE*

A:Map position: 81 min

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

C:Keywords: aminoacyltransferase; coenzyme A; cysteine biosynthesis

F:84-244/Domain: serine acetyltransferase homology <SAT>

Query Match 39.5%; Score 648.5; DB 1; Length 273;
Best Local Similarity 50.8%; Pred. No. 2e-46;

Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;

OY 43 EDDDDVWIKMLEAKSDVKQEPILSNYYASTSHRSLESAHLISVKSINLPSNTL 102

Db 4 EELEIWMNNIKAEARLADCEPMLASFYHATLKHENLGSALSYMLANKSSIPMPALAI 63

OY 103 FELFISVLEESPEIESTKODLAVKERDPACISYVHCFGLFACQAHRIHTLMQ 162

Db 64 REVEEAYAADPEMTIASACDIOAVRTDPADVDKSTPLLYLKGHALQATRIHWMIMQ 123

OY 163 NRKIVALLIONRVSESPAVNDIHPGAKIGKGLLDHATGVITGEPAVGDVNSILHGYTLG 222

Db 124 GRRLALIFLQOVSVTFQVDIHPAKIGKIGIMDHATGIVGFAVENDVSILQSVTLG 183

OY 223 GTGKSGDRHPRKIREGVMTGAGAKITLGNIEVGRKAGISGVVLQVPPTTAAGVPARI 282

Db 184 GTGKSGDRHPRKIREGVMTGAGAKITLGNIEVGRKAGISGVVLQVPPTTAAGVPARI 243

OY 283 IGGKENPRKHDKIPCLTMDQ 302

Db 244 VKKPS---DK-PSMDMDQ 258

RESULT 11

529568

serine O-acetyltransferase (EC 2.3.1.30) - *Salmonella typhimurium*

C:Species: *Salmonella typhimurium*

C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000

C:Accession: S29568

R:Submitted, A.V.; Kuczek, E.S.; Bawden, C.S.; Rogers, G.E.

submitted to the EMBL Data Library, May 1991

A:Description: A novel biosynthetic pathway for mammalian cells by stable integration of

A:Reference number: S29567

A:Accession: S29568

A:Molecule type: DNA

A:Residues: 1-273 <STV>

A:Cross-references: EMBL:X59594; NID:947659; PIDN:CAA42163.1; PID:947660

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

C:Keywords: acyltransferase; coenzyme A

F:84-244/Domain: serine acetyltransferase homology <SAT>

Query Match 39.5%; Score 648.5; DB 2; Length 273;
Best Local Similarity 51.2%; Pred. No. 2e-46;

Matches 133; Conservative 50; Mismatches 72; Indels 5; Gaps 2;

OY 43 EDDDDVWIKMLEAKSDVKQEPILSNYYASTSHRSLESAHLISVKSINLPSNTL 102

Db 4 EELEIWMNNIKAEARLADCEPMLASFYHATLKHENLGSALSYMLANKSSIPMPALAI 63

OY 103 FELFISVLEESPEIESTKODLAVKERDPACISYVHCFGLFACQAHRIHTLMQ 162

Db 64 REVEEAYAADPEMTIASACDIOAVRTDPADVDKSTPLLYLKGHALQATRIHWMIMQ 123

OY 163 NRKIVALLIONRVSESPAVNDIHPGAKIGKGLLDHATGVITGEPAVGDVNSILHGYTLG 222

Db 124 GRRLALIFLQOVSVTFQVDIHPAKIGKIGIMDHATGIVGFAVENDVSILQSVTLG 183

OY 223 GTGKSGDRHPRKIREGVMTGAGAKITLGNIEVGRKAGISGVVLQVPPTTAAGVPARI 282

Db 184 GTGKSGDRHPRKIREGVMTGAGAKITLGNIEVGRKAGISGVVLQVPPTTAAGVPARI 243

OY 283 IGGKENPRKHDKIPCLTMDQ 302

Db 244 VKKPS---DK-PSMDMDQ 258

RESULT 12

F86036

serine acetyltransferase [imported] - *Escherichia coli* (strain O157:H7)

C:Species: *Escherichia coli*

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C:Accession: F86036

R:Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

hiller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Djmalanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F86036

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-273 <STO>

A:Cross-references: GB:AE005174; NID:912518357; P:ON:AAG58754.1; GSPDB:GN00145; UMGCP:

A:Experimental source: strain O157:H7, substrain H:JL933

C:Genetics:

A:Gene: *cysE*

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

Query Match

Best Local Similarity 39.5%; Score 648.5; DB 2; Length 273;
Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;

OY 43 EDDDDVWIKMLEAKSDVKQEPILSNYYASTSHRSLESAHLISVKSINLPSNTL 102

Db 4 EELEIWMNNIKAEARLADCEPMLASFYHATLKHENLGSALSYMLANKSSIPMPALAI 63

OY 103 FELFISVLEESPEIESTKODLAVKERDPACISYVHCFGLFACQAHRIHTLMQ 162

Db 64 REVEEAYAADPEMTIASACDIOAVRTDPADVDKSTPLLYLKGHALQATRIHWMIMQ 123

OY 163 NRKIVALLIONRVSESPAVNDIHPGAKIGKGLLDHATGVITGEPAVGDVNSILHGYTLG 222

Db 124 GRRLALIFLQOVSVTFQVDIHPAKIGKIGIMDHATGIVGFAVENDVSILQSVTLG 183

OY 223 GTGKSGDRHPRKIREGVMTGAGAKITLGNIEVGRKAGISGVVLQVPPTTAAGVPARI 282

Db 184 GTGKSGDRHPRKIREGVMTGAGAKITLGNIEVGRKAGISGVVLQVPPTTAAGVPARI 243

OY 283 IGGKENPRKHDKIPCLTMDQ 302

Db 244 VKKPS---DK-PSMDMDQ 258

RESULT 13

G82049

serine acetyltransferase VC2649 [imported] - *Vibrio cholerae* (strain N16961 serogroup

C:Species: *Vibrio cholerae*

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: G82049

R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Chaiton, R.A.; Gwin, M.L.; Dodson, R.

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bess, S.; Qin, H.; Dragol, I.; Sellers

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; MUID:20406833

